

# Introducing MAPpoly2 and updates on QTLpoly: Supplementary Slides

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# MAPpoly2

## GitHub page and Rpubs

- <https://github.com/mmollina/mappoly2>
- [https://rpubs.com/mmollin/tutorial\\_mappoly2](https://rpubs.com/mmollin/tutorial_mappoly2)
- [https://rpubs.com/mmollin/multi\\_family\\_simulation](https://rpubs.com/mmollin/multi_family_simulation)

# Inter-connected tetraploid alfalfa families



Genetic  
Resources

ORIGINAL ARTICLE

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<https://www.genresj.org>

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## A public mid-density genotyping platform for alfalfa (*Medicago sativa* L.)

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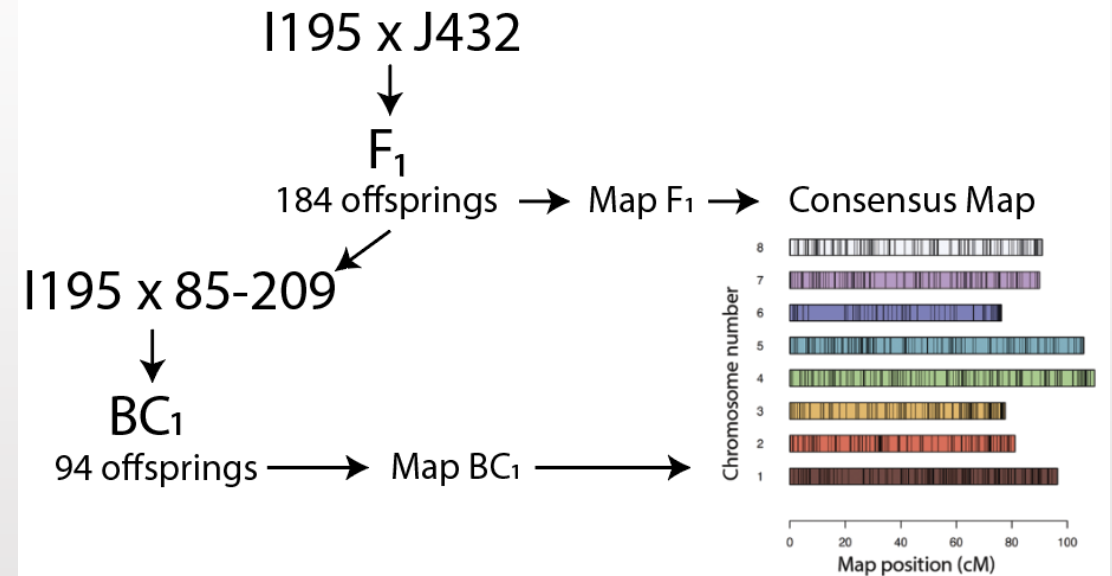
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<sup>c</sup> Campus Box 7609, North Carolina University, NC, Raleigh, 27695, USA

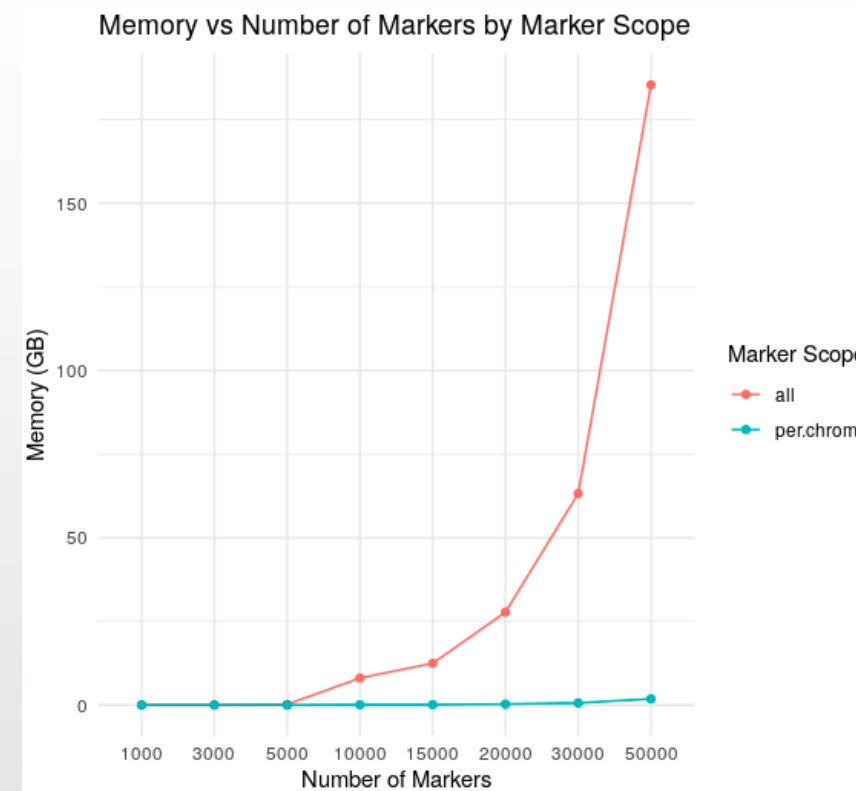
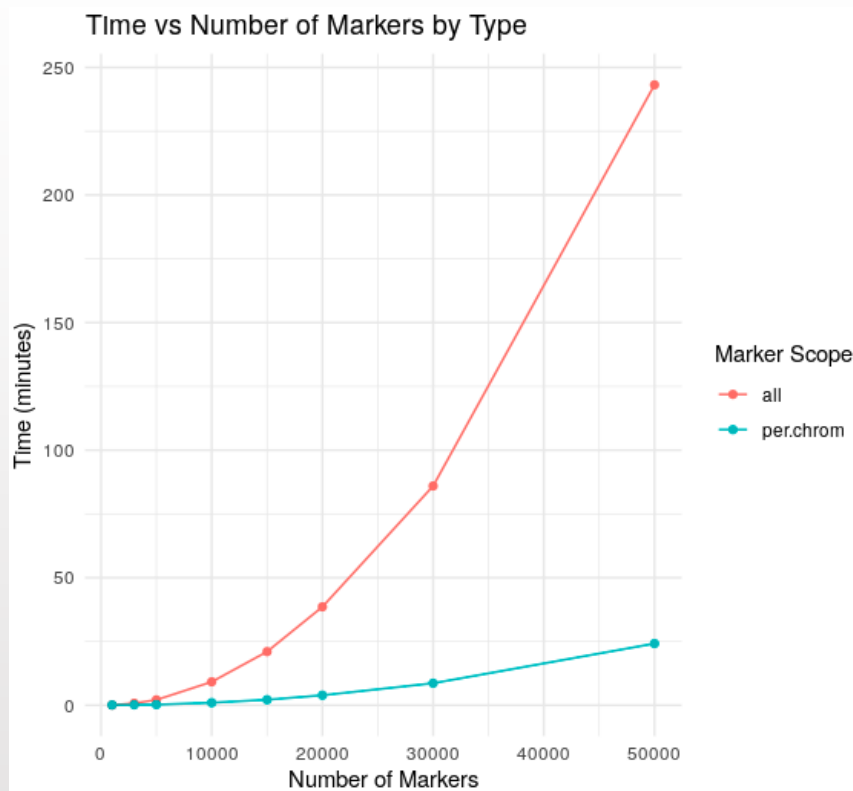
<sup>d</sup> Plant Science Research Unit, USDA-ARS, St. Paul, 55108, MN, USA

<sup>e</sup> Plant Germplasm Introduction and Testing Research Unit, USDA-ARS, Prosser, 99350, WA, USA

<sup>f</sup> Diversity Arrays Technology, ACT 2617, Bruce, Australia



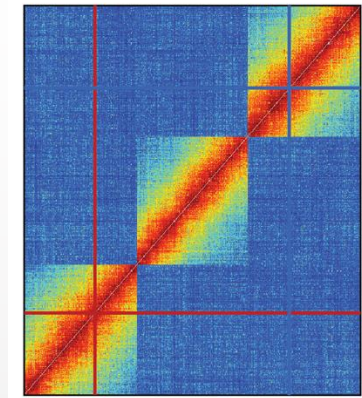
# Pairwise recombination – Time and Memory



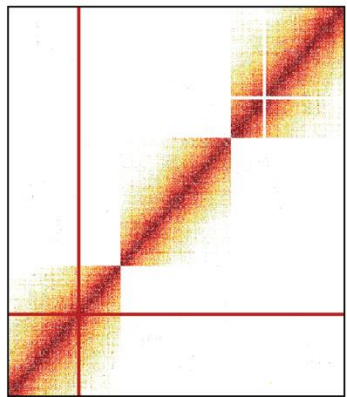
The simulation results showcased in this Figure were obtained using an Intel(R) Xeon(R) Gold 6226R CPU running at 2.90GHz, combined with 376 GB of RAM and 32 processing cores.

10 chromosomes

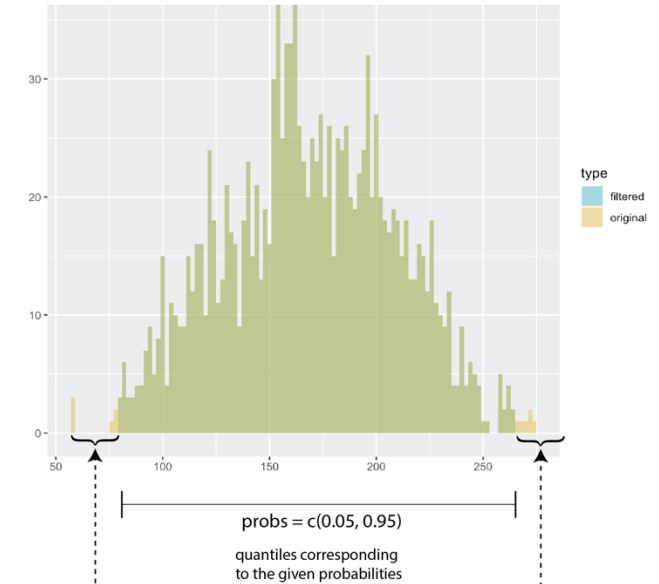
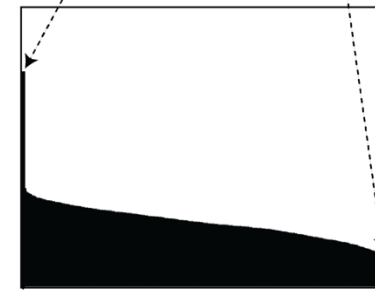
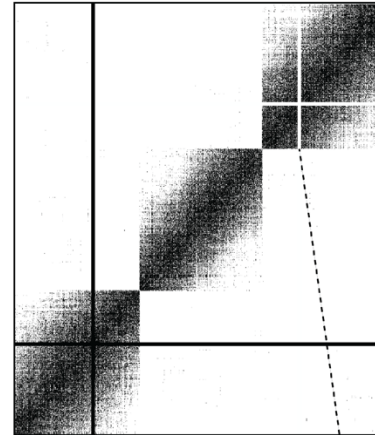
# Recombination fraction-based filtering



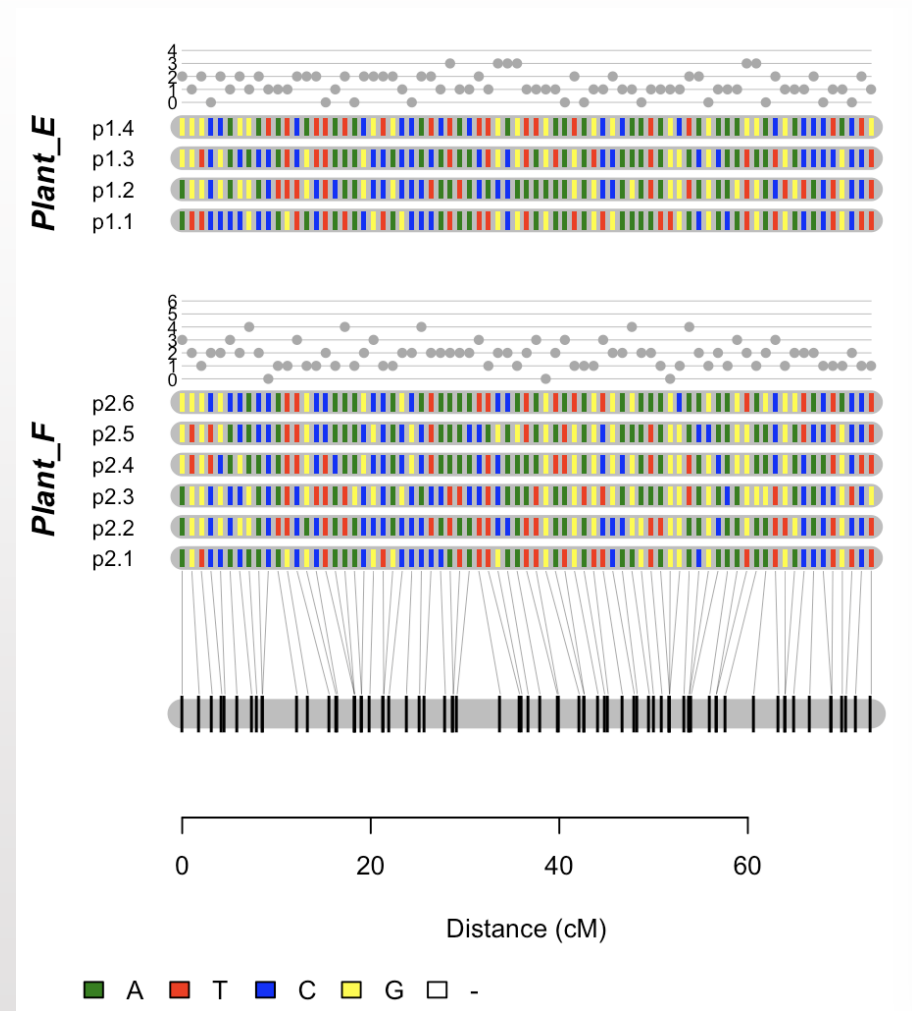
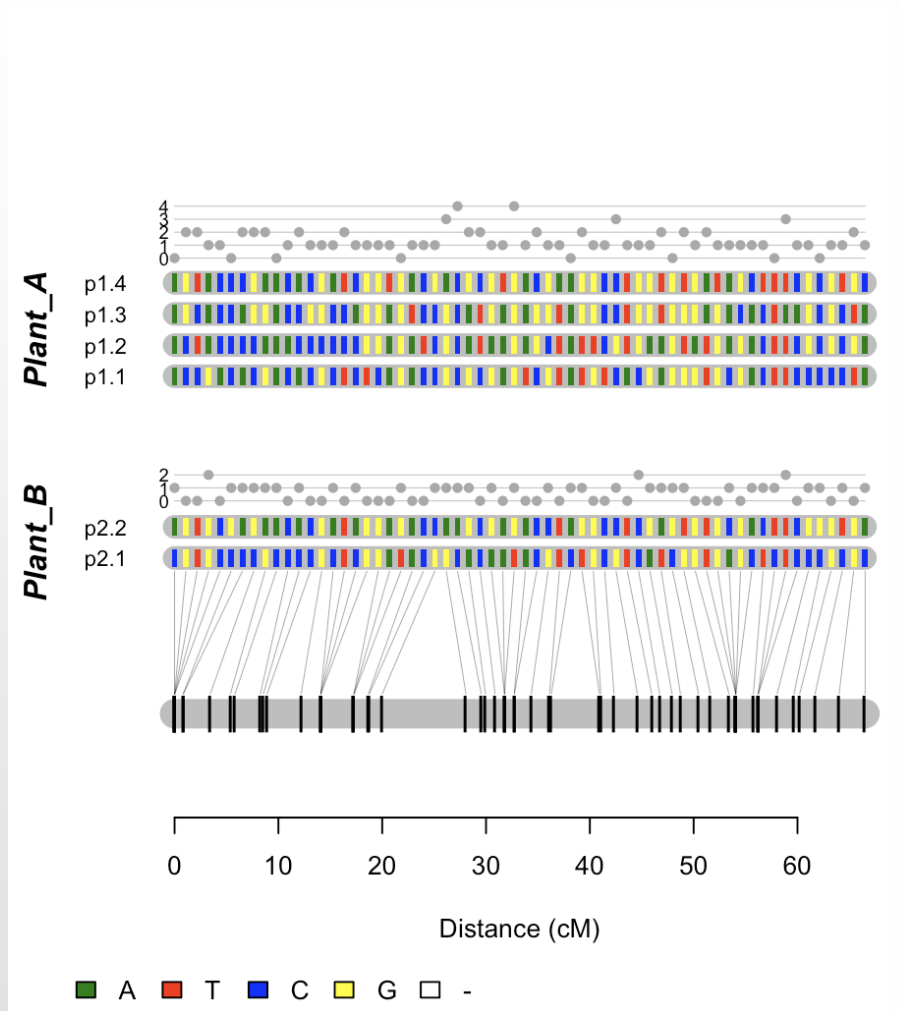
Screening parameters  
thresh.LOD.ph = 3 (statistical support for phase)  
thresh.LOD.rf = 3 (statistical support for recombination)  
thresh.rf = 0.25 (recombination threshold)



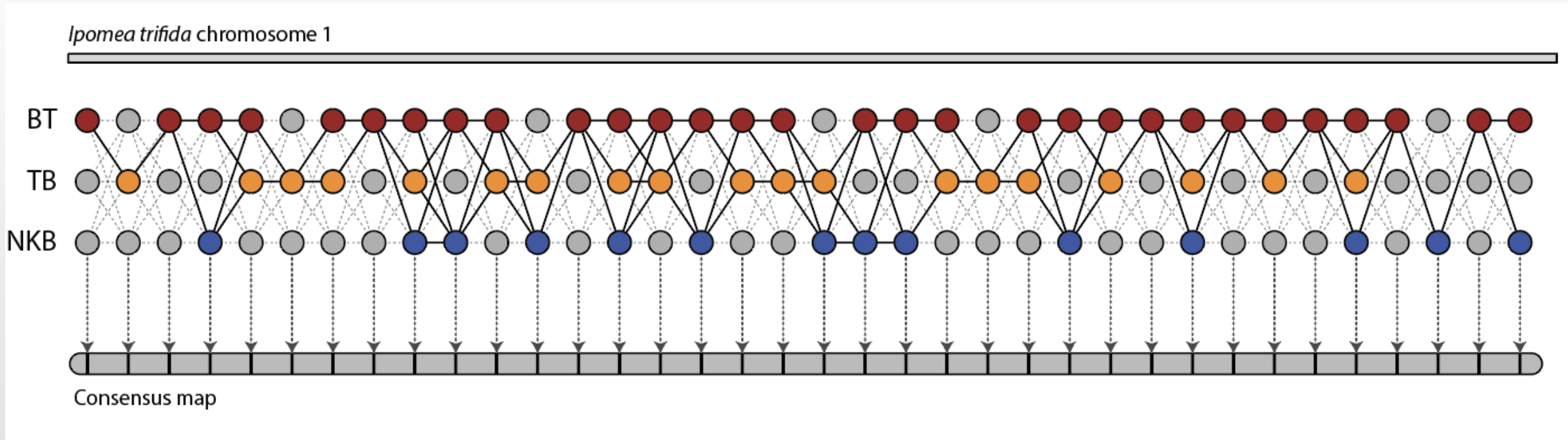
Binarization



# Mixed-ploidy cross: 4 x 2 and 6 x 4



# HMM and propagation of information in multiple maps



# Seven populations, 6 parents, 3 ploidy levels

Consensus Map:

Ploidy of founders: 4 2 4 2 4 6  
 Total No. individuals: 1400  
 Total No. markers: 981  
 Haplotype probability computed: No

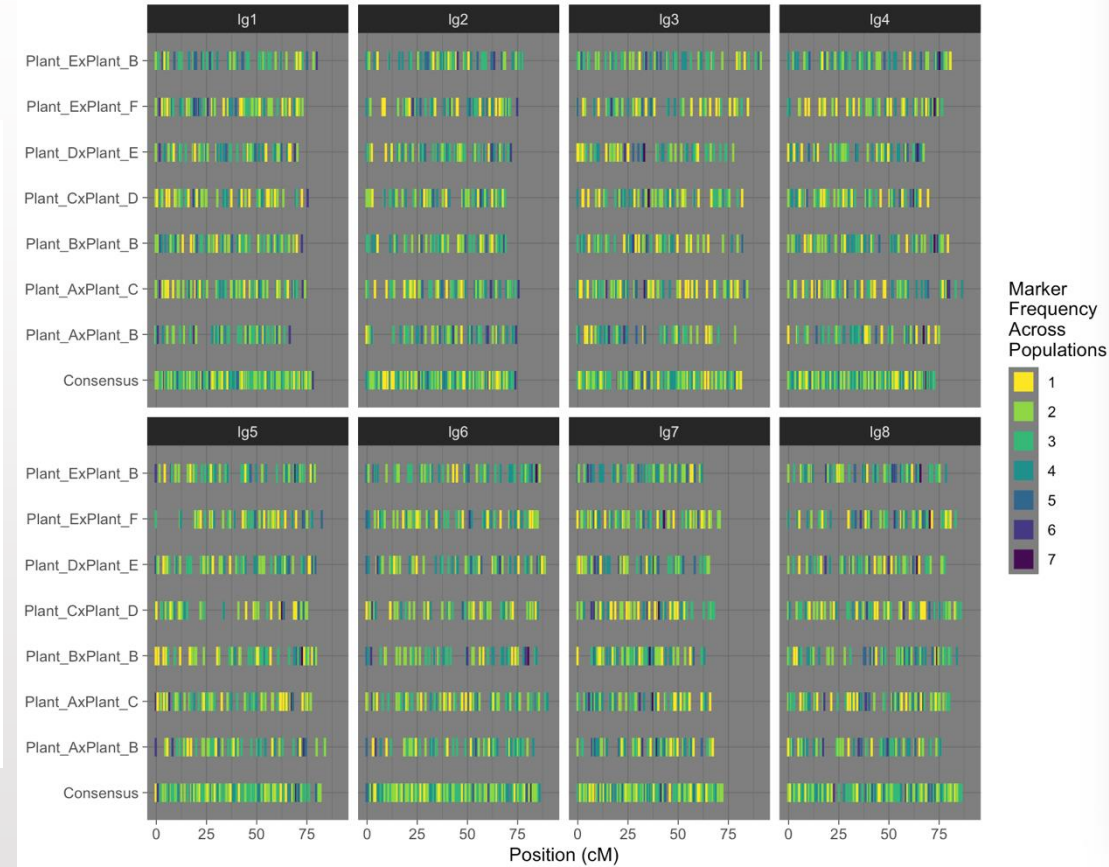
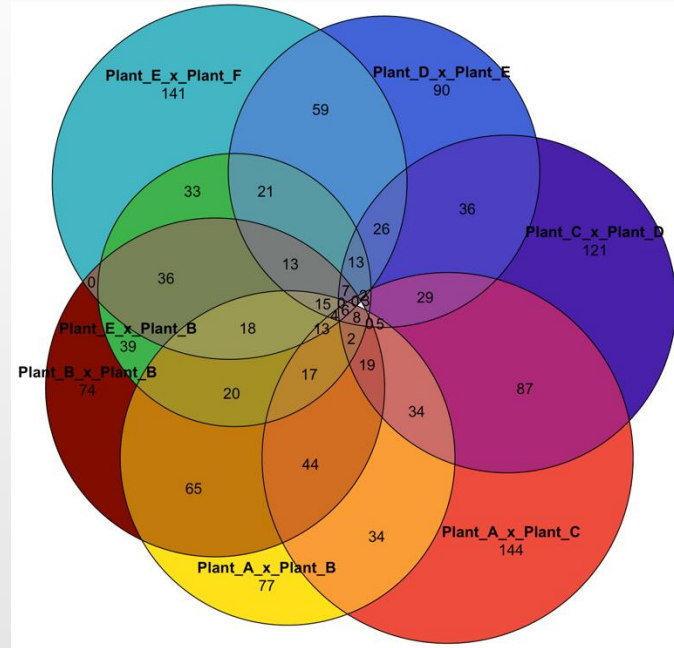
Number of individuals per crose:

	Plant_B	Plant_C	Plant_D	Plant_E	Plant_F
Plant_A	200	200	.	.	.
Plant_B	200	.	.	.	.
Plant_C	.	.	200	.	.
Plant_D	.	.	.	200	.
Plant_E	200	.	.	.	200

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Consensus Map:

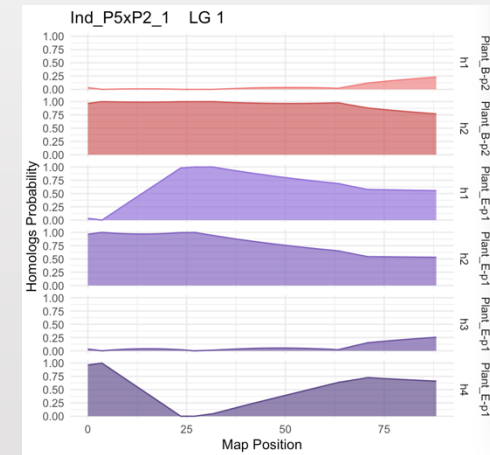
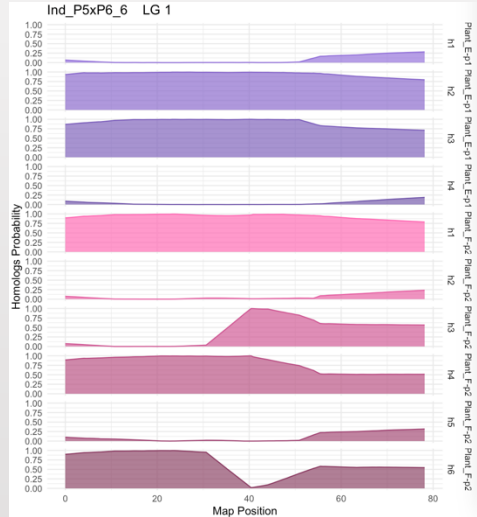
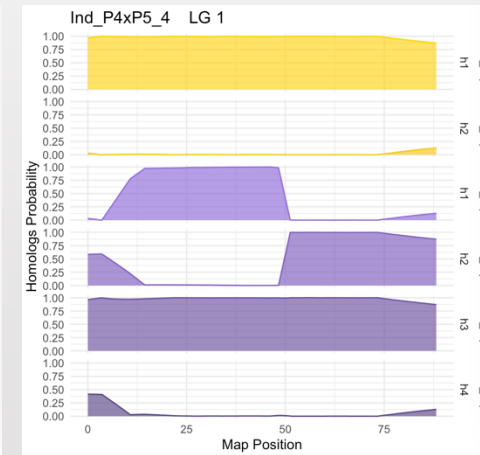
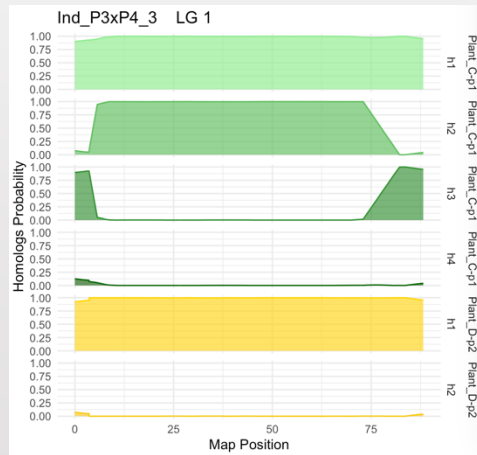
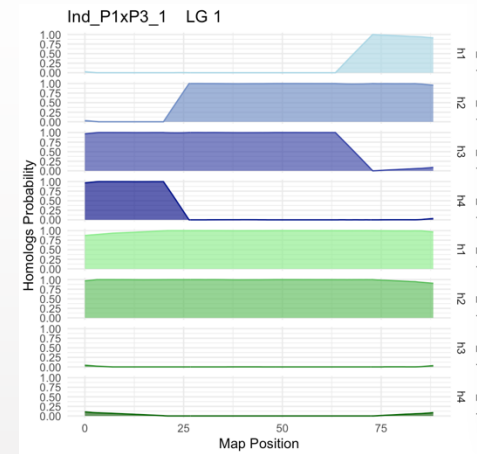
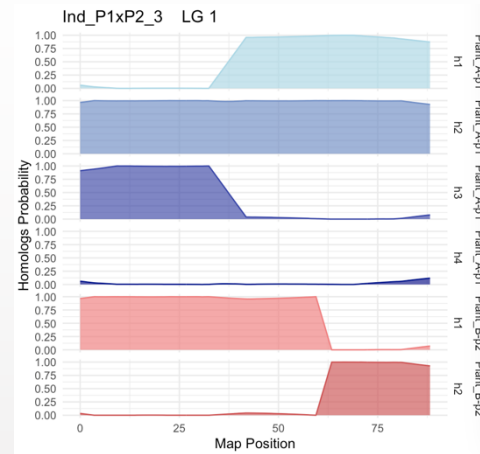
LG	Map_length_.cM.	Markers.cM	Total.mrk	Max_gap
lg1	78.15	1.599	125	1.09
lg2	73.96	1.677	124	1.06
lg3	81.58	1.483	121	3.65
lg4	72.93	1.659	121	1.11
lg5	81.9	1.404	115	3.36
lg6	86.12	1.428	123	1.67
lg7	72.08	1.734	125	1.99
lg8	86.3	1.472	127	2.43





# Haplotype probabilities

- Plant A
- Plant B
- Plant C
- Plant D
- Plant E
- Plant F



# Project Members



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# Other Collaborators



Neuhouse Farms



Wolf Roses L.L.C.



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